Robinson

1600

```
        RAW SEQUENCE LISTING              DATE: 02/11/2003
        PATENT APPLICATION:  US/09/659,379   TIME: 20:10:26

        Input Set : N:\Crf3\RULE60\09659379.txt
        Output Set: N:\CRF4\02112003\I659379.raw

        SEQUENCE LISTING
  3  (1) GENERAL INFORMATION:
  5      (i) APPLICANT: Vinik, Aaron
  6               . Pittenger, Gary
  7                   Rafaeloff-Phail, Ronit
  8                   Barlow, Scott
 10     (ii) TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
 11                       INGAP IN BACTERIAL AND EUKARYOTIC CELLS
 13    (iii) NUMBER OF SEQUENCES: 6
 15     (iv) CORRESPONDENCE ADDRESS:
 16          (A) ADDRESSEE: Banner & Witcoff, Ltd.
 17          (B) STREET: 1001 G Street, N.W.
 18          (C) CITY: Washington
 19          (D) STATE: DC
 20          (E) COUNTRY: USA
 21          (F) ZIP: 20001
 23      (v) COMPUTER READABLE FORM:
 24          (A) MEDIUM TYPE: Diskette
 25          (B) COMPUTER: IBM Compatible
 26          (C) OPERATING SYSTEM: DOS
 27          (D) SOFTWARE: FastSEQ for Windows Version 2.0
 29     (vi) CURRENT APPLICATION DATA:
C--> 30         (A) APPLICATION NUMBER: US/09/659,379
C--> 31         (B) FILING DATE: 08-Sep-2000
 32          (C) CLASSIFICATION:
 34    (vii) PRIOR APPLICATION DATA:
W--> 35         (A) APPLICATION NUMBER: US/08/909,725
 36          (B) FILING DATE: 12-AUG-1997
W--> 37         (A) APPLICATION NUMBER: 08/741,096
 38          (B) FILING DATE: 30-OCT-1996
 42   (viii) ATTORNEY/AGENT INFORMATION:
 43          (A) NAME: Kagan, Sarah A
 44          (B) REGISTRATION NUMBER: 32,145
 45          (C) REFERENCE/DOCKET NUMBER: 0570.05173
 47     (ix) TELECOMMUNICATION INFORMATION:
 48          (A) TELEPHONE: 202-508-9100
 49          (B) TELEFAX: 202-508-9299
 50          (C) TELEX: 97430 BMB UT
 53  (2) INFORMATION FOR SEQ ID NO: 1:
 55      (i) SEQUENCE CHARACTERISTICS:
 56          (A) LENGTH: 94 base pairs
 57          (B) TYPE: nucleic acid
 58          (C) STRANDEDNESS: single
```

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```
59          (D) TOPOLOGY: linear
62     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64  CTGCAAGACA GGTACCATGA TGCTTCCCAT GACCCTCTGT AGGATGTCTT GGATGCTGCT        60
65  TTCCTGCCTG ATGTTCCTTT CTTGGGTGGA AGGT                                   94
67  (2) INFORMATION FOR SEQ ID NO: 2:
69      (i) SEQUENCE CHARACTERISTICS:
70          (A) LENGTH: 31 base pairs
71          (B) TYPE: nucleic acid
72          (C) STRANDEDNESS: single
73          (D) TOPOLOGY: linear
76     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
78  CCGCGGATCC CGAAGAATCT CAAAAGAAAC T                                      31
80  (2) INFORMATION FOR SEQ ID NO: 3:
82      (i) SEQUENCE CHARACTERISTICS:
83          (A) LENGTH: 32 base pairs
84          (B) TYPE: nucleic acid
85          (C) STRANDEDNESS: single
86          (D) TOPOLOGY: linear
89     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
91  GACCGGCTCG AGTGCTCTTC CTGAGTGAAT CC                                     32
93  (2) INFORMATION FOR SEQ ID NO: 4:
95      (i) SEQUENCE CHARACTERISTICS:
96          (A) LENGTH: 558 base pairs
97          (B) TYPE: nucleic acid
98          (C) STRANDEDNESS: single
99          (D) TOPOLOGY: linear
101     (ii) MOLECULE TYPE: cDNA
103     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
105  CCGCGGATCC CGAAGAATCT CAAAAGAAAC TGCCTTCTTC ACGTATAACC TGTCCTCAAG        60
106  GCTCTGTAGC CTATGGGTCC TATTGCTATT CACTGATTTT GATACCACAG ACCTGGTCTA       120
107  ATGCAGAACT ATCCTGCCAG ATGCATTTCT CAGGACACCT GGCATTTCTT CTCAGTACTG       180
108  GTGAAATTAC CTTCGTGTCC TCCCTTGTGA AGAACAGTTT GACGGCCTAC CAGTACATCT       240
109  GGATTGGACT CCATGATCCC TCACATGGTA CACTACCCAA CGGAAGTGGA TGGAAGTGGA       300
110  GCAGTTCCAA TGTGCTGACC TTCTATAACT GGGAGAGGAA CCCCTCTATT GCTGCTGACC       360
111  GTGGTTATTG TGCAGTTTTG TCTCAGAAAT CAGGTTTTCA GAAGTGGAGA GATTTAATT        420
112  GTGAAAATGA GCTTCCCTAT ATCTGCAAAT TCAAGGTCTA GGGCAGTTCT AATTTCAACA       480
113  GCTTGAAAAT ATTATGAAGC TCACATGGAC AAGGAAGCAA GTATGAGGAT TCACTCAGGA       540
114  AGAGCACTCG AGCCGGTC                                                     558
116  (2) INFORMATION FOR SEQ ID NO: 5:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 26 amino acids
120          (B) TYPE: amino acid
121          (C) STRANDEDNESS: single
122          (D) TOPOLOGY: linear
124     (ii) MOLECULE TYPE: peptide
126     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
128  Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
129  1               5                   10                  15
130  Cys Leu Met Phe Leu Ser Trp Val Glu Gly
```

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131             20              25
133 (2) INFORMATION FOR SEQ ID NO: 6:
135     (i) SEQUENCE CHARACTERISTICS:
136         (A) LENGTH: 175 amino acids
137         (B) TYPE: amino acid
138         (C) STRANDEDNESS: single
139         (D) TOPOLOGY: linear
141   (ii) MOLECULE TYPE: protein
143   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
145 Met Met Leu Pro Met Thr Leu Cys Arg Met Ser Trp Met Leu Leu Ser
146  1               5                  10                  15
147 Cys Leu Met Phe Leu Ser Trp Val Glu Gly Glu Glu Ser Gln Lys Lys
148             20                  25                  30
149 Leu Pro Ser Ser Arg Ile Thr Cys Pro Gln Gly Ser Val Ala Tyr Gly
150             35                  40                  45
151 Ser Tyr Cys Tyr Ser Leu Ile Leu Ile Pro Gln Thr Trp Ser Asn Ala
152      50                  55                  60
153 Glu Leu Ser Cys Gln Met His Phe Ser Gly His Leu Ala Phe Leu Leu
154  65                  70                  75                  80
155 Ser Thr Gly Glu Ile Thr Phe Val Ser Ser Leu Val Lys Asn Ser Leu
156             85                  90                  95
157 Thr Ala Tyr Gln Tyr Ile Trp Ile Gly Leu His Asp Pro Ser His Gly
158             100                 105                 110
159 Thr Leu Pro Asn Gly Ser Gly Trp Lys Trp Ser Ser Ser Asn Val Leu
160             115                 120                 125
161 Thr Phe Tyr Asn Trp Glu Arg Asn Pro Ser Ile Ala Ala Asp Arg Gly
162      130                 135                 140
163 Tyr Cys Ala Val Leu Ser Gln Lys Ser Gly Phe Gln Lys Trp Arg Asp
164  145                 150                 155                 160
165 Phe Asn Cys Glu Asn Glu Leu Pro Tyr Ile Cys Lys Phe Lys Val
166             165                 170                 175
```

VERIFICATION SUMMARY   DATE: 02/11/2003
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)